




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#11 Search **BRCA2 fusion protein**

11:48:00 22

#10 Search **RAD51 fusion protein**

11:47:26 74

#7 Search **#5 and structure**

11:47:08 9

#9 Search **fds**

11:45:52 404

#6 Search **#5 and crystal and structure**

09:31:29 2

#5 Search **RAD51-BRC**

09:31:15 31

#2 Search **#1 and crystal**

09:17:51 2

#1 Search **RAD51 and BRC**

09:17:08 31

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		<i>DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI; PLUR=YES; OP=ADJ</i>	
<input type="checkbox"/>	L5	RAD51 and (venkitaraman\$ or pellegrini\$ or blundell\$ or yu\$ or bates\$).in.	18
<input type="checkbox"/>	L4	RAD51 and BRC and "crystal".clm.	1
<input type="checkbox"/>	L3	L1 and "crystal".clm.	0
<input type="checkbox"/>	L2	L1 and crystal	14
<input type="checkbox"/>	L1	RAD51 and BRCA	40

END OF SEARCH HISTORY

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(FILE 'HOME' ENTERED AT 13:04:12 ON 13 JUN 2007)

FILE 'CAPLUS' ENTERED AT 13:04:53 ON 13 JUN 2007

L1 34 S RAD51 AND BRC

L2 4 S L1 AND CRYSTAL

=> d L2 1-4

L2 ANSWER 1 OF 4 CAPLUS COPYRIGHT 2007 ACS on STN

AN 2004:354973 CAPLUS

DN 140:334412

TI Use of crystal structure of human RAD51-BRCA2  
BRC repeat complex in screening for anti tumor agents

IN Venkitaraman, Ashok; Pellegrini, Luca; Blundell, Tom; Yu, David; Lo,  
Thomas; Bates, Debbie; Shivji, Mahmud; Anand, Shubha; Lee, Miyoung

PA Cambridge University Technical Services Ltd., UK

SO PCT Int. Appl., 102 pp.

CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2004035621	A2	20040429	WO 2003-GB4485	20031014
	WO 2004035621	A3	20040826		
	AU 2003271967	A1	20040504	AU 2003-271967	20031014
	EP 1551871	A2	20050713	EP 2003-753806	20031014
	EP 1650223	A2	20060426	EP 2005-26068	20031014
	EP 1650223	A3	20060726		
	US 2006234293	A1	20061019	US 2005-531242	20050524
PRAI	GB 2002-23860	A	20021014		
	EP 2003-753806	A3	20031014		
	WO 2003-GB4485	W	20031014		

L2 ANSWER 2 OF 4 CAPLUS COPYRIGHT 2007 ACS on STN

AN 2003:705265 CAPLUS

DN 140:72789

TI Sequence fingerprints in BRCA2 and RAD51: implications for DNA  
repair and cancer

AU Lo, Thomas; Pellegrini, Luca; Venkitaraman, Ashok R.; Blundell, Tom L.

CS Department of Biochemistry, University of Cambridge, Cambridge, CB2 1GA,  
UK

SO DNA Repair (2003), 2(9), 1015-1028

CODEN: DRNEAR; ISSN: 1568-7864

PB Elsevier Science B.V.

DT Journal

LA English

RE.CNT 61. THERE ARE 61 CITED REFERENCES AVAILABLE FOR THIS RECORD  
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 3 OF 4 CAPLUS COPYRIGHT 2007 ACS on STN

AN 2003:681788 CAPLUS

DN 139:318901

TI Full-length archaeal Rad51 structure and mutants: mechanisms for  
RAD51 assembly and control by BRCA2

AU Shin, David S.; Pellegrini, Luca; Daniels, Douglas S.; Yelent, Biana;  
Craig, Lisa; Bates, Debbie; Yu, David S.; Shivji, Mahmud K.; Hitomi,  
Chiharu; Arvai, Andrew S.; Volkmann, Niels; Tsuruta, Hiro; Blundell, Tom

L.; Venkitaraman, Ashok R.; Tainer, John A.  
CS Department of Molecular Biology and The Skaggs Institute for Chemical  
Biology, The Scripps Research Institute, La Jolla, CA, 92037, USA  
SO EMBO Journal (2003), 22(17), 4566-4576  
CODEN: EMJODG; ISSN: 0261-4189  
PB Oxford University Press  
DT Journal  
LA English  
RE.CNT 42 THERE ARE 42 CITED REFERENCES AVAILABLE FOR THIS RECORD  
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 4 OF 4 CAPLUS COPYRIGHT 2007 ACS on STN  
AN 2002:883768 CAPLUS  
DN 138:200905  
TI Insights into DNA recombination from the structure of a RAD51  
-BRCA2 complex  
AU Pellegrini, Luca; Yu, David S.; Lo, Thomas; Anand, Shubha; Lee, MiYoung;  
Blundell, Tom L.; Venkitaraman, Ashok R.  
CS Department of Biochemistry, University of Cambridge, Cambridge, CB2 1GA,  
UK  
SO Nature (London, United Kingdom) (2002), 420(6913), 287-293  
CODEN: NATUAS; ISSN: 0028-0836  
PB Nature Publishing Group  
DT Journal  
LA English  
RE.CNT 35 THERE ARE 35 CITED REFERENCES AVAILABLE FOR THIS RECORD  
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1n0w



DOI 10.2210/pdb1n0w/pdb

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**Title** Crystal structure of a RAD51-BRCA2  
BRC repeat complex**Authors** Pellegrini, L., Yu, D.S., Lo,  
T., Anand, S., Lee, M., Blundell,  
T.L., Venkitaraman, A.R.**Primary Citation**Pellegrini, L., Yu, D.S., Lo, T., Anand,  
S., Lee, M., Blundell,  
T.L., Venkitaraman, A.R. Insights into  
DNA recombination from the structure of a  
RAD51-BRCA2 complex *Nature* v420  
pp.287-293, 2002

[Abstract]

**History**Deposition 2002-10-15 Release 2002-  
11-27**Experimental  
Method**Type X-RAY DIFFRACTION Data   
[EDS]**Parameters**

Resolution [Å]	R-Value	R-Free	Space Group
1.70	0.191 (work)	0.206	P 2 <sub>1</sub> 2 <sub>1</sub> 2 <sub>1</sub>

**Unit Cell**

Length [Å]	a	57.30	b	59.14	c	77.20
Angles [°]	alpha	90.00	beta	90.00	gamma	90.00

**Molecular  
Description  
Asymmetric Unit**

Polymer: 1 Molecule: DNA repair protein  
RAD51 homolog 1 Fragment: ATPase  
domain Chains: A  
Polymer: 2 Molecule: Breast cancer type 2  
susceptibility protein Fragment: BRC  
repeat type 4 Chains: B  
Polymer: 3 Molecule: peptide linker  
Chains: L Other Details: this peptide links  
the BRCA2 to the RAD51  
Polymer: 4 Molecule: ARTIFICIAL GLY-  
SER-MSE-GLY PEPTIDE Chains: C  
Other Details: this peptide comes from the  
expression vector and is linked to the N-  
terminus of BRCA2

■ 1N0W

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Structure Analysis

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Displa

MBT Pi

### Classification Gene Regulation/antitumor Protein

#### Source

Polymer: 1 Scientific Name: **Homo sapiens** Common Name: **Human**  
 Polymer: 2 Scientific Name: **Escherichia coli** Common Name: **Escherichia coli**  
 Expression system: **Escherichia coli**  
 Unknown Expression system: **Escherichia coli**  
 Unknown Expression system: **Escherichia coli**

#### Chemical Component

Identifier Name	Formula	Drug Similarity	He
MSE SELENOMETHIONINE	$C_5 H_{11} N O_2$ Se		
MG MAGNESIUM ION	$Mg^{2+}$		
EDO 1,2-ETHANEDIOL	$C_2 H_6 O_2$		
CL CHLORIDE ION	$Cl^-$		

#### SCOP Classification (version 1.71)

Domain Info	Class	Fold	Superfamily	Family
d1n0wa_	Alpha and beta proteins (a/b)	P-loop containing nucleoside triphosphate hydrolases	P-loop containing nucleoside triphosphate hydrolases	RecA protein-like (ATPase-domain)
d1n0wb_	Peptides	BRCA2 BRC4 repeat	BRCA2 BRC4 repeat	BRCA2 BRC4 repeat

#### CATH Classification (version v3.0.0)

Domain	Class	Architecture	Topology
1n0wA00	Alpha Beta	3-Layer(aba) Sandwich	Rossmann

#### PFAM Classification

Chain	PFAM Accession	PFAM ID	Description	Type
A	PF08423	Rad51	Rad51	Dom
B	PF00634	BRCA2	BRCA2 repeat	Fam

#### GO Terms

Polymer	Molecular Function	Biological Process
DNA repair protein RAD51 homolog 1 (1N0W:A)	<ul style="list-style-type: none"> <li>nucleotide binding</li> <li>nucleotide binding</li> <li>DNA binding</li> <li>DNA binding</li> <li>damaged DNA binding</li> <li>damaged DNA binding</li> <li>ATP binding</li> <li>ATP binding</li> <li>DNA-dependent ATPase activity</li> <li>DNA-dependent ATPase</li> </ul>	<ul style="list-style-type: none"> <li>DNA metabolic process</li> <li>DNA metabolic process</li> <li>DNA repair</li> <li>DNA repair</li> </ul>

Breast cancer type 2  
susceptibility protein  
(1N0W:B)  
peptide linker (1N0W:L)  
ARTIFICIAL GLY-SER-  
MSE-GLY PEPTIDE  
(1N0W:C)

- activity
- nucleoside-triphosphatase activity
- nucleoside-triphosphatase activity

- none
- none
- none
- DNA repair
- DNA repair
- none
- none



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☐ 1: [P42212](#). Reports Green fluorescent...[gi:1169893]BLink, Conserved  
Domains, Links[Comment](#) [Features](#) [Sequence](#)

LOCUS [P42212](#) 238 aa linear INV 01-MAY-2007

DEFINITION [Green fluorescent protein.](#)

ACCESSION [P42212](#)

VERSION [P42212](#) [GI:1169893](#)

DBSOURCE [swissprot: locus GFP\\_AEQVI, accession \[P42212\]\(#\);](#)  
[class: standard.](#)  
[extra accessions: Q17104, Q27903](#)  
[created: Nov 1, 1995.](#)  
[sequence updated: Nov 1, 1995.](#)  
[annotation updated: May 1, 2007.](#)  
[xrefs: M62654.1, AAA27722.1, M62653.1, AAA27721.1, L29345.1,](#)  
[AAA58246.1, X96418.1, CAA65278.1, JQ1514, 1B9CA, 1B9CB, 1B9CC,](#)  
[1B9CD, 1BFP @, 1C4FA, 1CV7A, 1EMA @, 1EMB @, 1EMCA, 1EMCB, 1EMCC,](#)  
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[1GFLA, 1GFLB, 1H6RA, 1H6RB, 1H6RC, 1HCJA, 1HCJB, 1HCJC, 1HCJD,](#)  
[1HUYA, 1JBYA, 1JBZA, 1JC0A, 1JC0B, 1JC0C, 1JC1A, 1JC1B, 1JC1C,](#)  
[1KP5A, 1KP5B, 1KYPA, 1KYRA, 1KYSA, 1MYWA, 1Q4AA, 1Q4BA, 1Q4CA,](#)  
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[1W7TB, 1W7TC, 1W7TD, 1W7UA, 1W7UB, 1W7UC, 1W7UD, 1YFPA, 1YFPB,](#)  
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[2B3QC, 2B3QD, 2EMD @, 2EMN @, 2EMO @, 2FWQA, 2FZUA, 2G16A, 2G2SB,](#)  
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[GO: 0006091, InterPro: IPR009017, InterPro: IPR011584,](#)  
[InterPro: IPR000786, Gene3D: G3DSA: 2.40.155.10, Pfam: PF01353,](#)  
[PRINTS: PR01229, ProDom: PD013756](#)

KEYWORDS 3D-structure; Chromophore; Direct protein sequencing; Luminescence;  
Photoprotein.

SOURCE [Aequorea victoria](#)

ORGANISM [Aequorea victoria](#)  
[Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;](#)  
[Aequoreidae; Aequorea.](#)

REFERENCE 1 (residues 1 to 238)

AUTHORS [Prasher, D.C., Eckenrode, V.K., Ward, W.W., Prendergast, F.G. and](#)  
[Cormier, M.J.](#)

TITLE [Primary structure of the Aequorea victoria green-fluorescent](#)  
[protein](#)

JOURNAL [Gene 111 \(2\), 229-233 \(1992\)](#)

PUBMED [1347277](#)

REMARK [NUCLEOTIDE SEQUENCE \[MRNA\], AND PARTIAL PROTEIN SEQUENCE.](#)

REFERENCE 2 (residues 1 to 238)

AUTHORS [Inouye, S. and Tsuji, F.I.](#)

TITLE [Aequorea green fluorescent protein. Expression of the gene and](#)



fluorescence characteristics of the recombinant protein  
JOURNAL FEBS Lett. 341 (2-3), 277-280 (1994)  
PUBMED [8137953](#)  
REMARK NUCLEOTIDE SEQUENCE [MRNA].  
REFERENCE 3 (residues 1 to 238)  
AUTHORS Rouwendal, G.J., Mendes, O., Wolbert, E.J. and Douwe de Boer, A.  
TITLE Enhanced expression in tobacco of the gene encoding green  
fluorescent protein by modification of its codon usage  
JOURNAL Plant Mol. Biol. 33 (6), 989-999 (1997)  
PUBMED [9154981](#)  
REMARK NUCLEOTIDE SEQUENCE [MRNA].  
REFERENCE 4 (residues 1 to 238)  
AUTHORS Cody, C.W., Prasher, D.C., Westler, W.M., Prendergast, F.G. and  
Ward, W.W.  
TITLE Chemical structure of the hexapeptide chromophore of the Aequorea  
green-fluorescent protein  
JOURNAL Biochemistry 32 (5), 1212-1218 (1993)  
PUBMED [8448132](#)  
REMARK CHROMOPHORE.  
REFERENCE 5 (residues 1 to 238)  
AUTHORS Ormo, M., Cubitt, A.B., Kallio, K., Gross, L.A., Tsien, R.Y. and  
Remington, S.J.  
TITLE Crystal structure of the Aequorea victoria green fluorescent  
protein  
JOURNAL Science 273 (5280), 1392-1395 (1996)  
PUBMED [8703075](#)  
REMARK X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).  
REFERENCE 6 (residues 1 to 238)  
AUTHORS Yang, F., Moss, L.G. and Phillips, G.N. Jr.  
TITLE The molecular structure of green fluorescent protein  
JOURNAL Nat. Biotechnol. 14 (10), 1246-1251 (1996)  
PUBMED [9631087](#)  
REMARK X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).  
REFERENCE 7 (residues 1 to 238)  
AUTHORS Wachter, R.M., Elsliger, M.A., Kallio, K., Hanson, G.T. and  
Remington, S.J.  
TITLE Structural basis of spectral shifts in the yellow-emission variants  
of green fluorescent protein  
JOURNAL Structure 6 (10), 1267-1277 (1998)  
PUBMED [9782051](#)  
REMARK X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF MUTANT WITH YELLOW  
EMISSION.  
REFERENCE 8 (residues 1 to 238)  
AUTHORS Elsliger, M.A., Wachter, R.M., Hanson, G.T., Kallio, K. and  
Remington, S.J.  
TITLE Structural and spectral response of green fluorescent protein  
variants to changes in pH  
JOURNAL Biochemistry 38 (17), 5296-5301 (1999)  
PUBMED [10220315](#)  
REMARK X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
COMMENT On Apr 26, 2005 this sequence version replaced [gi:7428731](#).  
[FUNCTION] Energy-transfer acceptor. Its role is to transduce the  
blue chemiluminescence of the protein aequorin into green  
fluorescent light by energy transfer. Fluoresces in vivo upon  
receiving energy from the Ca(2+)-activated photoprotein aequorin.  
[BIOPHYSICOCHEMICAL PROPERTIES] Absorption: Abs(max)=395 nm;  
Note=Exhibits a smaller absorbance peak at 470 nm. The fluorescence  
emission spectrum peaks at 509 nm with a shoulder at 540 nm.  
[SUBUNIT] Monomer.  
[TISSUE SPECIFICITY] Photocytes.  
[PTM] Contains a chromophore consisting of modified amino acid  
residues. The chromophore is formed by autocatalytic backbone  
condensation between Xaa-N and Gly-(N+2), and oxidation of

Tyr-(N+1) to didehydrotyrosine. Maturation of the chromophore requires nothing other than molecular oxygen.

[BIOTECHNOLOGY] Fluorescent proteins have become a useful and ubiquitous tool for making chimeric proteins, where they function as a fluorescent protein tag. Typically they tolerate N- and C-terminal fusion to a broad variety of proteins. They have been expressed in most known cell types and are used as a noninvasive fluorescent marker in living cells and organisms. They enable a wide range of applications where they have functioned as a cell lineage tracer, reporter of gene expression, or as a measure of protein-protein interactions.

[SIMILARITY] Belongs to the GFP family.

[WEB RESOURCE] NAME=Protein Spotlight; NOTE=The greenest of us all - Issue 11 of June 2001;

URL=[http://www.expasy.org/spotlight/back\\_issues/sptlt011.shtml](http://www.expasy.org/spotlight/back_issues/sptlt011.shtml)'.

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<u>Region</u>	5..228 /gene="GFP" /region_name="GFP" /note="Green fluorescent protein; pfam01353" /db_xref="CDD:65172"
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<u>Region</u>	37..39

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Bond /gene="GFP"  
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181 hyqqntpigd gpvllpdnhy lstqsalskd pnekrdhmv1 lefvtaagit hgmdelyk

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☐ 1: CAA64484, Reports brca2 [Homo sapie...[gi:1177438]BLink, Conserved  
Domains, LinksFeatures Sequence

LOCUS CAA64484 3418 aa linear PRI 14-NOV-2006

DEFINITION brca2 [Homo sapiens].

ACCESSION CAA64484

VERSION CAA64484.1 GI:1177438

DBSOURCE embl accession X95152.1embl accession X95153.1embl accession X95154.1embl accession X95155.1embl accession X95156.1embl accession X95157.1embl accession X95158.1embl accession X95159.1embl accession X95160.1embl accession X95161.1embl accession X95162.1embl accession X95163.1embl accession X95164.1embl accession X95165.1embl accession X95166.1embl accession X95167.1embl accession X95168.1embl accession X95169.1embl accession X95170.1embl accession X95171.1embl accession X95172.1embl accession X95173.1embl accession X95174.1embl accession X95175.1embl accession X95176.1embl accession X95177.1

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiensEukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;  
Catarrhini; Hominidae; Homo.

REFERENCE

1

AUTHORS

Wooster,R., Bignell,G., Lancaster,J., Swift,S., Seal,S.,  
Mangion,J., Collins,N., Gregory,S., Gumbs,C., Micklem,G.,  
Barfoot,R., Hamoudi,R., Patel,S., Rice,C., Biggs,P., Hashim,Y.,  
Smith,A., Connor,F., Arason,A., Gudmundsson,J., Ficenece,D.,  
Kelsell,D., Ford,D., Tonin,P., Bishop,D.T., Spurr,N.K.,  
Ponder,B.A.J., Eeles,R., Peto,J., Devilee,P., Cornelisse,C.,  
Lynch,H., Narod,S., Lenoir,G., Egilsson,V., Barkadottir,R.B.,  
Easton,D.F., Bentley,D.R., Futreal,P.A., Ashworth,A. and

Stratton,M.R.  
TITLE Identification of the breast cancer susceptibility gene BRCA2  
JOURNAL Nature 378 (6559), 789-792 (1995)  
PUBMED 8524414  
REMARK Erratum: [Nature 1996 Feb 22;379(6567):749]  
REFERENCE 2 (residues 1 to 3418)  
AUTHORS Wooster,R.  
TITLE Direct Submission  
JOURNAL Submitted (15-JAN-1996) R. Wooster, Institute of Cancer Research,  
Haddow Labs, 15 Cotswold Rd, Sutton, Surrey, SM2 5NG, UK

FEATURES  
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/db\_xref="CDD:72965"

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2814..3054

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/db\_xref="CDD:72966"

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#### ORIGIN

Repeated Sequence

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121 ktkmdqaddv scpllncsfc espvvlqcth vtpqrdrksvv cgslfhtpkf vkgrqtpkhi
181 seslgaevdp dmswssslat pptlsstvli vrneeasetv fphdttanvk syfsnhdesl
241 kkndrfiasv tdsentnqre aashgfgkts gnsfkvnscck dhigksmpnv ledevyetvv
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841 rvaspsrkqv fnqntnlrvi qknqeetst1 skitvnpdse elfsdnennf v1qvanernn
901 lalntkelh etdltcvnep ifknstmvly gdtgdkqatq vsikkdlvyv laeenknsvk
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1381 ked1sdl1tfl evakaqeach gntsnkeq1t atkteqnikd fetsd1tffqt asgkn1svak
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2881 tkpylpsral trqqvralqd gaelyeavkn aadpaylegy fseeqlraln nhrqmlndkk  
2941 qaqiqleirk amesaeqkeq glsrdvttvw klrvsyskk ekdsvisliw rpssdylsll  
3001 tegkryriyh latsksksks eraniqlaat kktqyqqlpv sdeilfqiyq preplhfskf  
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3361 qfisvsestr taptssedyl rlkrcttsl ikeqessqas teeceknkqd titttkkyi

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☐ 1: AAA43099. Reports hemagglutinin [In...[gi:323995]BLink, Conserved  
Domains, LinksFeatures Sequence

LOCUS AAA43099 566 aa linear VRL 13-JUL-2006  
 DEFINITION hemagglutinin [Influenza A virus (A/Udorn/307/1972 (H3H2))].  
 ACCESSION AAA43099  
 VERSION AAA43099.1 GI:323995  
 DBSOURCE locus FLADORNHA accession M54895.1  
 KEYWORDS  
 SOURCE Influenza A virus (A/Udorn/307/1972 (H3H2))  
 ORGANISM Influenza A virus (A/Udorn/307/1972 (H3H2))  
 Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
 Influenzavirus A.  
 REFERENCE 1 (residues 1 to 566)  
 AUTHORS Iuferov, V.P., Karginov, V.A., Samokhvalov, E.I., Chizhikov, V.E. and  
 Vasilenko, S.K.  
 TITLE Nucleotide sequence of the hemagglutinin gene of the influenza  
 virus A/Udorn/307/72 (H3N2)  
 JOURNAL Dokl. Akad. Nauk SSSR 278 (3), 738-742 (1984)  
 PUBMED 6548691  
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